

corrected 70235USPCT.ST25
SEQUENCE LISTING

<110> Brown, Devon
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Heifetz, Peter B.

<120> Expression in plants of antibodies against enterotoxigenic
Escherichia coli

<130> 70235USPCT

<140> 10/544,284
<141> 2005-08-02

<150> PCT/EP2004/001427
<151> 2004-02-16

<150> US 60/448,429
<151> 2003-02-18

<160> 80

<170> PatentIn version 3.3

<210> 1
<211> 399
<212> DNA
<213> artificial sequence

<220>
<223> codon optimised

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aagctctcct gcgccgcctc cggttcacc ttctccgact acttcatgtc ctggattcgc 120
cagaccccggaagaagcgcct ggagtgggtc gccaccatca acaacggcgg ctcccacacc 180
tactgctccg acaacgtgaa gggccgcttc accaccttcc gcgacaacgt gaagaacacc 240
ctctacctcc agatgtcctc cctcaacttc gaggacaccg ccatgtacta ctgcgcccgc 300
gcctactacc gcttcgacgt gcgcgcctgg ttctcctact ggggccaggg caccctcgtg 360
accgtgtcca cggccaagac caccgcccgc tccgtctac 399

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<211> 582
<212> DNA
<213> artificial sequence

<220>
<223> codon optimised

<400> 2
agtgcacatc tcctcaccca gtccccggcc atcctctcca tgatcccgcg ccagcgcgtg 60
tccttctcct gccgcgcctc ccagatcatc ggcaccacca tccactgggtc ccagcagcgc 120

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accgacggct ccccgcgctt cctcatccag tgcgcctccg agtccatctc cggcatcccc	180
tccccgtttt ccggcaccgg ctccggcacc gacttcaccc tcaacttcaa ctccgtggag	240
tccgagtaca tcaccgacta ctactgccag cagtccaaca cctggccgac ctaccggtt	300
ggcggcgcca ccaagctcga gatcaagcgc gccgacgccg ccccgaccgt gtccatcttc	360
ccgcccgtct ccgagcagct cacctccggc ggcgcgctcc tgggtgtgctt cctcaacaac	420
ttctaccgga aggacatcaa cgtgaagtgg aagatcgacg gctccgagcg ccagaacggc	480
gtgctcaact cctggaccga ccaggactcc aaggactcca cctactccat gtcctccacc	540
ctcaccctca ccaaggacga gtacgagcgc cacaactcct ac	582

<210> 3
 <211> 399
 <212> DNA
 <213> mouse

<400> 3	
actagtgaag tgcaactggg ggagtctggg ggaggcttcg tgaagcctgg agggctccctg	60
aaactctcct gtgcagcctc tggattcact ttcagtgact atttcattgtc ttggattcgc	120
cagactccgg aaaagagggt ggagtgggtc gcaaccatta ataatgggtg tagtcacacc	180
tactgttcag acaatgtgaa gggacgattt acaactttca gagacaatgt caaaaacacc	240
ctgtaccttc aaatgagcag tctgaacttt gaggacacag ccatgtatta ctgtgcaaga	300
gcctactata gggtcgacgt gagggcctgg ttttcttatt ggggccaagg gactctgggtc	360
actgtctcta cagccaaaac gacaccccca tctgtctac	399

<210> 4
 <211> 330
 <212> DNA
 <213> mouse

<400> 4	
actagtgaca tcttgctgac tcagtctcca gccatcctgt ctatgattcc aagacaaaga	60
gtcagtttct cctgcagggc cagtcagatc attggcacia ccatacactg gtctcagcaa	120
agaacagatg gttctcctag gcttctcata cagtgtgctt ctgagtctat ctctgggatc	180
ccttcagggt ttagtggcac tggatcaggg acagatttta ctcttaactt caacagtgtg	240
gagtctgaat atattacaga ttattactgt caacaaagta atacctggcc aacgtacccg	300
ttcggagggg ggaccaagct cgagataaaa	330

<210> 5
 <211> 396
 <212> DNA
 <213> artificial sequence

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<220>

<223> codon optimised

<400> 5

actagtgacg tgcagctcgt ggagtccggc ggcggcctcg tgcagccggg cggctcccgc	60
aagctctcct gcgccgcctc cggcttcacc ttctcctcct tcgccatgca ctgggtgcgc	120
caggccccag agaagggcct ggagtgggtg gcctacatct cctccggctc catcaccatc	180
tactacgccg acaccgtgaa gggccgcttc accgtgtccc gcgacaaccc gaagtccacc	240
ctcttcctcc agatgacctc cctccgcagc gaggacaccg ccatgtacta ctgcgcccgc	300
gacgactacg gtcctccgg ctggtacttc gacgtctggg gcgctggcac cacggtgacc	360
gtgtcctcgg ccaagaccac cccgccgtcc gtctac	396

<210> 6

<211> 336

<212> DNA

<213> artificial sequence

<220>

<223> codon optimised

<400> 6

actagtgaca tcgtgatgtc ccagtccccg tcctccctcg ccgtgtccgc tggcgagaag	60
gtcaccatgt cctgcaagtc ctcccagtc ctctcaact cccgcacccg caagaactac	120
ctcgctggt atcagcagaa gccgggccag tccccgaagc tcctcatcta ctgggcctcc	180
acccgcgagt ccggcggtgcc ggaccgcttc accggctccg gtcccggcac cgacttcacc	240
ctcaccatct cctccgtgca ggcggaggac ctcgccgtgt actactgcac ccagtcctac	300
aacctcctca ccttcggcgc cggtaccaag ctcgag	336

<210> 7

<211> 393

<212> DNA

<213> artificial sequence

<220>

<223> anti0k88 codon optimised VH from 36-41

<400> 7

actagtgagg tccagctgca gcagtctgga cctgaactag tgaagactgg ggcttcagtg	60
aagatattct gcaaggcttc tgattactca ctactgatt actacatgca ctgggtcaag	120
cagagccatg gagagagcct tgagtggatt ggatatatta atttttacaa tgggtgtact	180
aactacaacc agaagttcaa gggcaaggcc acatttactg tagacacatc ctccagcaca	240
gtctacatgc agttcaacag cctgacatct gaagactctg cggcttatta ttgtgtaaga	300
gaagcattac tacggaacta tgctatggac tactgggggtc aaggaacctc agtcaccgtc	360
tcctcagcca aaacgacacc cccatctgtc tac	393

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<210> 8
 <211> 324
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti0K88 codon optimised VL from 36-41

<400> 8
 actagtgaaa atgtgctcac ccagtctcca gcaatcatgt ctgcatctcc aggggaaaag 60
 gtcacatga cctgcagggc cagctcaagt gtaagttccc gttacttgca ctggtaccag 120
 cagaagtcag gtgcctcccc caaactctgg atttatagca catccaactt ggcttctgga 180
 gtccctgctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagt 240
 gtggaggctg aagatgctgc cacttattac tgccagcaat acagtgggta cccgtggacg 300
 ttcggtggag gcaccaagct cgag 324

<210> 9
 <211> 408
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti0K88 codon optimised VH from 7-46

<400> 9
 actagtgaag tgaagcttga ggagtctgga ggaggcttgg tgcaacctgg aggatccatg 60
 agactctcct gtgttgccctc tggattcact ttcagtaact actggatgaa ctgggtccgc 120
 cagtctccag agaaggggct tgagtgggtt gctgaaatta gattgacatc taataatttt 180
 gcaacacatt atgcggagtc tgtgaaaggg aggttcacca tctcaagaga tgattccaaa 240
 agtagtgtct acctgcaa atgaacaactta agagctgaag aactggcat ttattactgt 300
 accaggcctt actacggtgg taggttcttc tactgggtact tcgatgtctg gggcgcaggg 360
 accacggtca ccgtctcctc aacaaaaacg acaccccat ctgtctac 408

<210> 10
 <211> 324
 <212> DNA
 <213> artificial sequence

<220>
 <223> anti-K88 codon optimised VL from 7-46

<400> 10
 actagtgaaa ttgtgctcac ccagtctcca accaccatgg ctgcatctcc cggggagaag 60
 atcactatca cctgcagtgc cagctcaagt ataagttcca attacttgca ttggtatcag 120
 cagaagccag gattctcccc taaactcttg atttatagga catccaatct ggcttctgga 180

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gtcccagttc gcttcagtgg cagtgggtct gggacctctt actctctcac aattggcacc 240
 atggaggctg aagatgttgc cacttactac tgccagcagg gtaatagtat accattcacg 300
 ttcggctcgg ggacaaagct cgag 324

<210> 11
 <211> 363
 <212> DNA
 <213> mouse

<400> 11
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 tcctgtgcag cctctggatt cactttcagt agctttgcaa tgcactgggt tcgtcaggct 120
 ccagagaagg ggctggagtg ggtcgcatat attagtagtg gcagtattac catctactat 180
 gcagacacag tgaagggccg attcacctgc tccagagaca atcccaagag caccctgttc 240
 ctgcaaatga ccagtctaag gtctgaggac acggccatgt attactgtgc aagagacgac 300
 tacggtagta gcgggtggta cttcgatgtc tggggcgag ggaccacggt caccgtctcc 360
 tca 363

<210> 12
 <211> 350
 <212> DNA
 <213> mouse

<400> 12
 gacattgtga tgtcacagtc tccatcctcc ctggctgtgt cagcaggaga gaaggtcact 60
 atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct 120
 tggtagcagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg 180
 gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cacyctcacc 240
 atcagcagtg tgcaggctga agacctggca gtttattact gcacgcaatc ttataatctg 300
 ctcacgttcg gtgctgggac caagctggaa ctgaatcggg ctgatgctgc 350

<210> 13
 <211> 410
 <212> DNA
 <213> mouse

<400> 13
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 catggagaga gccttgagtg gattggatat attaatTTTT acaatgggtgc tactaactac 180
 aaccagaagt tcaagggcaa ggccacattt actgtagaca catcctccag cacagtctac 240
 atgcagttca acagcctgac atctgaagac tctgcgggtct attattgtgt aagagaagca 300

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ttactacgga actatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca 360
gccccaaacga cccccccatc tgtctatcca ctggccccta ctagtgctgc 410

<210> 14
<211> 317
<212> DNA
<213> mouse

<400> 14
gaaaatgtgc tcaccagtc tccagcaatc atgtctgcat ctccagggga aaaggtcacc 60
atgacctgca gggccagctc aagtgttaagt tcccgttact tgcactggta ccagcagaag 120
tcagggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtcctt 180
gctcgcttca gtggcagtggt gtctgggacc tcttactctc tcacaatcag cagtgtggag 240
gctgaagatg ctgccactta ttactgccag caatacagtg gttaccctgtg gacgttcggt 300
ggaggcacca agctgga 317

<210> 15
<211> 374
<212> DNA
<213> mouse

<400> 15
gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgagactc 60
tcctgtgttg cctctggatt cactttcagt aactactgga tgaactgggt ccgccagtct 120
ccagagaagg ggcttgagtg ggttgctgaa attagattga catctaataa ttttgcaaca 180
cattatgcgg agtctgtgaa agggagggtc accatctcaa gagatgattc caaaagtagt 240
gtctacctgc aaatgaacaa cttaagagct gaagacactg gcatttatta ctgtaccagg 300
ccttactacg gtggtaggtt cttctactgg tacttcgatg tctggggcgc agggaccacg 360
gtcaccgtct cctc 374

<210> 16
<211> 318
<212> DNA
<213> mouse

<400> 16
gaaattgtgc tcaccagtc tccaaccacc atggctgcat ctcccgggga gaagatcact 60
atcacctgca gtgccagctc aagtataagt tccaattact tgcattggta tcagcagaag 120
ccaggattct cccctaaact cttgatttat aggacatcca atctggcttc tggagtccca 180
gttcgcttca gtggcagtggt gtctgggacc tcttactctc tcacaattgg caccatggag 240
gctgaagatg ttgccactta ctactgccag cagggttaata gtataccatt cacgttcggc 300
tcggggacaa agctcgag 318

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<210> 17
 <211> 134
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti-K99 heavy chain variable region

<400> 17

Ala Thr Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Phe Val Lys
 1 5 10 15

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30

Ser Asp Tyr Phe Met Ser Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu
 35 40 45

Glu Trp Val Ala Thr Ile Asn Asn Gly Gly Ser His Thr Tyr Cys Ser
 50 55 60

Asp Asn Val Lys Gly Arg Phe Thr Thr Phe Arg Asp Asn Val Lys Asn
 65 70 75 80

Thr Leu Tyr Leu Gln Met Ser Ser Leu Asn Phe Glu Asp Thr Ala Met
 85 90 95

Tyr Tyr Cys Ala Arg Ala Tyr Tyr Arg Phe Asp Val Arg Ala Trp Phe
 100 105 110

Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Ala Lys Thr
 115 120 125

Thr Pro Pro Ser Val Tyr
 130

<210> 18
 <211> 229
 <212> PRT
 <213> artificial sequence

<220>
 <223> anti0k99 light chain

<220>
 <221> misc_feature
 <222> (1)..(229)
 <223> X at positions 225 and 226 designates an unknown amino acid
 <400> 18

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Ala Thr Ser Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Met
1 5 10 15

Ile Pro Arg Gln Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ile Ile
20 25 30

Gly Thr Thr Ile His Trp Ser Gln Gln Arg Thr Asp Gly Ser Pro Arg
35 40 45

Leu Leu Ile Gln Cys Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg
50 55 60

Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Asn Phe Asn Ser
65 70 75 80

Val Glu Ser Glu Tyr Ile Thr Asp Tyr Tyr Cys Gln Gln Ser Asn Thr
85 90 95

Trp Pro Thr Tyr Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
210 215 220

Xaa Xaa Thr Gly Phe
225

<210> 19
<211> 29
<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 19

accatggatt ttcaagtgcg gattttcag

29

<210> 20

<211> 31

<212> DNA

<213> artificial sequence

<220>

<223> Primer MLALT3

<400> 20

caccatggag wcacakwctc agtgtctttr t

31

<210> 21

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> Primer MLALT4

<400> 21

caccatgkcc ccwrctcagy tyctkgt

27

<210> 22

<211> 28

<212> DNA

<213> artificial sequence

<220>

<223> Primer MLALT5

<400> 22

caccatgaag ttgcctgtta ggctgttg

28

<210> 23

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> Primer MH1

<400> 23

atatccacca tggratgsag ctgkgmtats ctctt

35

<210> 24

<211> 35

<212> DNA

<213> artificial sequence

<220>

<223> Primer MH2

<400> 24
atatccacca tgracttcgg gytgagctkg gtttt 35

<210> 25
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> primer 33615

<400> 25
gaagatctag acttactatg cagcatcagc 30

<210> 26
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> primer MVG1R

<400> 26
ggcagcacta gtaggggcca gtggata 27

<210> 27
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> Primer MVG2R

<400> 27
gaggarccac tagtatctcc acacmcaggg gccag 35

<210> 28
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> ER transit peptide

<400> 28
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser

<210> 29
<211> 24
<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 29

acgcgtcgat catccaggtg caac

24

<210> 30

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 30

actagtggcg ctcgcagcga ga

22

<210> 31

<211> 25

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 31

accggttctg ttctgcacaa agtgt

25

<210> 32

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> primer

<400> 32

acgcgtttgt acccctggat t

21

<210> 33

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> Primer

<400> 33

acgcgtttgc atgcctgcag tg

22

<210> 34

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> PRIMER

<400> 34

agtccaacgg tggagcggaa ct

22

<210> 35

<211> 6

<212> PRT

<213> artificial sequence

<220>

<223> ER retention signal

<400> 35

Ser Glu Lys Asp Glu Leu
1 5

<210> 36

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 36

agcttgatc cactagtacc ggtacgcgtg

30

<210> 37

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 37

aattcacgcg taccgtact agtgatcca

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<210> 38

<211> 72

<212> DNA

<213> artificial sequence

<220>

<223> oligonucleotide

<400> 38

catgtgaggc caccacaag acctccacct cccaatcgt gaagagcttc aaccgcaacg

60

agtgctgata ga

72

<210> 39

<211> 72

<212> DNA

<213> artificial sequence

<220>
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 <400> 39
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 tgggtggcct ca 72

<210> 40
 <211> 36
 <212> DNA
 <213> artificial sequence
 <220>
 <223> oligonucleotide
 <400> 40
 agcttacgcg tggatccact agtgagctcg gtaccg 36

<210> 41
 <211> 36
 <212> DNA
 <213> artificial sequence
 <220>
 <223> oligonucleotide
 <400> 41
 aattcggtag cgagctcact agtggatcca cgcgta 36

<210> 42
 <211> 54
 <212> DNA
 <213> artificial sequence
 <220>
 <223> oligonucleotide
 <400> 42
 ccgggcaagt ccgagaagga cgagctgtga taggagctca aggtaccgaa ttca 54

<210> 43
 <211> 54
 <212> DNA
 <213> artificial sequence
 <220>
 <223> oligonucleotide
 <400> 43
 agcttgaatt cggtaccttg agctcctatc acagctcgtc cttctcggac ttgc 54

<210> 44
 <211> 23
 <212> DNA
 <213> artificial sequence
 <220>

<223> primer

<400> 44

aagcagtggg atcaacgcag agt

23

<210> 45

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> primer SMART IIA

<400> 45

aagcagtggg atcaacgcag agtacgcggg

30

<210> 46

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> Primer K99HC-3'

<400> 46

aagtagacag atgggggtgt cg

22

<210> 47

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> Primer K88_746_VAR-H5'

<400> 47

gccactagtg aagtgaagct tgaggag

27

<210> 48

<211> 26

<212> DNA

<213> artificial sequence

<220>

<223> Primer K88_1744_VAR_H5'

<400> 48

gccactagtg atgtgcagct ggtgga

26

<210> 49

<211> 27

<212> DNA

<213> artificial sequence

<220>

<223> Primer K88_3641_VAR_H5'

<400> 49

gccactagtg aggtccagct gcagcag corrected 70235USPCT.ST25 27

<210> 50
 <211> 26
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer K88_746_VAR_L5

<400> 50
 ccactagtg aattgtgctc acccag 26

<210> 51
 <211> 28
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer K88_746_VAR_L3

<400> 51
 ttatctcgag ctttgtcccc gagccgaa 28

<210> 52
 <211> 27
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer K88_3641_VAR_L5

<400> 52
 gccactagtg aaaatgtgct cacccag 27

<210> 53
 <211> 28
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer K88_3641_VAR_L3

<400> 53
 ttatctcgag cttggtgcct ccaccgaa 28

<210> 54
 <211> 27
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer K88_1744_VAR_L5

<400> 54
 gccactagtg acattgtgat gtcacag 27

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<210> 55
 <211> 30
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer K88_1744_VAR_L3

<400> 55
 ttatctcgag cttggtccca gcaccgaacg

30

<210> 56
 <211> 5
 <212> PRT
 <213> artificial sequence

<220>
 <223> Light Chain Variable Domain Motif

<400> 56
 Lys Leu Glu Ile Lys
 1 5

<210> 57
 <211> 972
 <212> DNA
 <213> artificial sequence

<220>
 <223> Consensus nucleotide sequence of murine IgG1 heavy chain

<400> 57
 gccaaaacga ccccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 60
 tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 120
 tggaactctg gatccctgtc cagcgggtgtg cacaccttcc cagctgtcct gcagtctgac 180
 ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 240
 acctgcaacg ttgccacccc ggccagcagc accaagggtg acaagaaaat tgtgcccagg 300
 gattgtgggt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 360
 ccccaaagc ccaaggatgt gtcaccatt actctgactc ctaagggtcac gtgtgtttgtg 420
 gtagacatca gcaaggatga tcccagggtc cagttcagct ggttttaga tgatgtggag 480
 gtgcacacag ctgagacgca accccgggag gagcagttca acagcacttt ccgctcagtc 540
 agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttaa atgcagggtg 600
 aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg 660
 aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc 720
 agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtggt 780
 aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct 840

tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc 900
 acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctcccac 960
 tctcctggta aa 972

<210> 58
 <211> 39
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer for Human CH3

<400> 58
 gaattaagga tccaaagcca aaggccagcc ccgcgaacc 39

<210> 59
 <211> 38
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer for Human CH3

<400> 59
 tttattgatt attgctcgag tttacccgga gacagggga 38

<210> 60
 <211> 42
 <212> DNA
 <213> artificial sequence

<220>
 <223> primer for Murine CH3

<400> 60
 aattaatgaa ttaaggatcc aagaccaagg gccgcccga gg 42

<210> 61
 <211> 42
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer for Murine CH3

<400> 61
 tttattgatt attgctcgag cttgcccggg gagtgagaga gg 42

<210> 62
 <211> 38
 <212> DNA
 <213> artificial sequence

<220>
 <223> Primer for Bovine CH3

<400> 62
aattaatgaa ttaaggatcc cgcaccaaag gccctgcc 38

<210> 63
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> Primer for Bovine CH3

<400> 63
tttattgatt attgctcgag cttgccggcg gacttggagg 40

<210> 64
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Primer for Bovine CH2CH3

<400> 64
ttaatgaatt aaggatccgg cggcccatct gtgttcatct tc 42

<210> 65
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> primer for Bovine CH2CH3

<400> 65
tttattgatt attgctcgag cttgccggcg gacttggagg 40

<210> 66
<211> 230
<212> PRT
<213> artificial sequence

<220>
<223> Consensus amino acid sequence of IgG Fc sequences

<400> 66

His Cys Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
1 5 10 15

Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
20 25 30

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
35 40 45

Gln Pro Val Phe Ser Trp Tyr Val Asp Gly Val Glu Val His Thr Ala
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50

55

60

Lys Met Leu Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
65 70 75 80

Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu Asn Gly Lys
85 90 95

Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala Pro Ile Glu
100 105 110

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Glu Pro Gln Val
115 120 125

Tyr Val Leu Pro Pro Pro Arg Glu Glu Leu Ser Lys Asn Asp Thr Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Ala Val
145 150 155 160

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Asn Lys Tyr Lys Thr
165 170 175

Thr Pro Pro Gln Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
180 185 190

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Thr Phe Thr Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Lys Ser Pro Gly Lys
225 230

<210> 67
<211> 471
<212> PRT
<213> mouse

<400> 67

Thr Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala
1 5 10 15

Ser Ala Thr Ser Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
20 25 30

Gln Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
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35

Phe Ser Ser Phe Ala Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
50 55 60

Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ile Thr Ile Tyr Tyr
65 70 75 80

Ala Asp Thr Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Pro Lys
85 90 95

Ser Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala
100 105 110

Met Tyr Tyr Cys Ala Arg Asp Asp Tyr Gly Ser Ser Gly Trp Tyr Phe
115 120 125

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr
130 135 140

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
145 150 155 160

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
165 170 175

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
195 200 205

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
210 215 220

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
225 230 235 240

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
245 250 255

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
260 265 270

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
275 280 285

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Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
290 295 300

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
305 310 315 320

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
340 345 350

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
355 360 365

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
370 375 380

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
385 390 395 400

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
405 410 415

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
420 425 430

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
435 440 445

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
450 455 460

Lys Ser Glu Lys Asp Glu Leu
465 470

<210> 68
<211> 244
<212> PRT
<213> mouse

<400> 68

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
20 25 30

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Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
50 55 60

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
100 105 110

Cys Thr Gln Ser Tyr Asn Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu
225 230 235 240

Lys Asp Glu Leu

<210> 69
<211> 469
<212> PRT
<213> mouse

<400> 69

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30
 Thr Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Asp Tyr Ser Leu
 35 40 45
 Thr Asp Tyr Tyr Met His Trp Val Lys Gln Ser His Gly Glu Ser Leu
 50 55 60
 Glu Trp Ile Gly Tyr Ile Asn Phe Tyr Asn Gly Ala Thr Asn Tyr Asn
 65 70 75 80
 Gln Lys Phe Lys Gly Lys Ala Thr Phe Thr Val Asp Thr Ser Ser Ser
 85 90 95
 Thr Val Tyr Met Gln Phe Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Val Arg Glu Ala Leu Leu Arg Asn Tyr Ala Met Asp Tyr
 115 120 125
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 130 135 140
 Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 145 150 155 160
 Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 165 170 175
 Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 180 185 190
 Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 195 200 205
 Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 210 215 220
 His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 225 230 235 240
 Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 245 250 255

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Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
260 265 270

Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
275 280 285

Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
290 295 300

Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
305 310 315 320

Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
325 330 335

Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
340 345 350

Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
355 360 365

Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
370 375 380

Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
385 390 395 400

Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
405 410 415

Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
420 425 430

Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
435 440 445

His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ser
450 455 460

Glu Lys Asp Glu Leu
465

<210> 70
<211> 240
<212> PRT
<213> mouse

<400> 70

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15
Ala Thr Ser Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
20 25 30
Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
35 40 45
Ser Ser Arg Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro
50 55 60
Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
85 90 95
Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
100 105 110
Gly Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
130 135 140
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
145 150 155 160
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
165 170 175
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
180 185 190
Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
195 200 205
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
210 215 220
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
225 230 235 240

<210> 71
<211> 474

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<212> PRT
<213> mouse

<400> 71

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Gly Ser Met Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
35 40 45

Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
50 55 60

Glu Trp Val Ala Glu Ile Arg Leu Thr Ser Asn Asn Phe Ala Thr His
65 70 75 80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
85 90 95

Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr
100 105 110

Gly Ile Tyr Tyr Cys Thr Arg Pro Tyr Tyr Gly Gly Arg Phe Phe Tyr
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
130 135 140

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
145 150 155 160

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
165 170 175

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
195 200 205

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
210 215 220

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
225 230 235 240

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Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
245 250 255

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
260 265 270

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
275 280 285

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
290 295 300

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
305 310 315 320

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
340 345 350

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
355 360 365

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
370 375 380

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
385 390 395 400

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
405 410 415

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
420 425 430

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
435 440 445

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
450 455 460

Ser Pro Gly Lys Ser Glu Lys Asp Glu Leu
465 470

<210> 72

corrected 70235USPCT.ST25

<211> 268
<212> PRT
<213> mouse

<400> 72

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser Glu Ile Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
20 25 30

Ser Pro Gly Leu Tyr Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser
35 40 45

Ser Ile Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Leu
50 55 60

Tyr Phe Ser Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser
65 70 75 80

Gly Leu Tyr Val Pro Val Arg Phe Ser Gly Leu Tyr Ser Gly Leu Tyr
85 90 95

Ser Gly Leu Tyr Thr Ser Tyr Ser Leu Thr Ile Gly Leu Tyr Thr Met
100 105 110

Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Leu Tyr Asn
115 120 125

Ser Ile Pro Phe Thr Phe Gly Leu Tyr Ser Gly Leu Tyr Thr Lys Leu
130 135 140

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
145 150 155 160

Ser Ser Glu Gln Leu Thr Ser Gly Leu Tyr Gly Leu Tyr Ala Ser Val
165 170 175

Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp
180 185 190

Lys Ile Asp Gly Leu Tyr Ser Glu Arg Gln Asn Gly Leu Tyr Val Leu
195 200 205

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
210 215 220

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr

corrected 70235USPCT.ST25

225 230 235 240

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
245 250 255

Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
260 265

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<210> 73
<211> 10
<212> PRT
<213> artificial sequence
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<220>
<223> Predicted N-terminal Sequence of 36/41 VL

<400> 73

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
1 5 10

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<210> 74
<211> 9
<212> PRT
<213> artificial sequence
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<220>
<223> obtained N-terminal of 36/41 VL
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<400> 74

Val Arg Leu Thr Gln Ser Pro Ala Ile
1 5

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<210> 75
<211> 10
<212> PRT
<213> artificial sequence
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<220>
<223> Predicted N-terminal sequence of 36/41 VH

<400> 75

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10

<210>	76
<211>	10
<212>	PRT
<213>	artificial sequence

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<220>
<223>  obtained N-terminal sequence of 36/41 VH
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<400> 76

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 1 5 10

<210> 77
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> Predicted N-terminal sequence of 36/41 derived VL produced in Cor
 <400> 77

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
 1 5 10

<210> 78
 <211> 9
 <212> PRT
 <213> artificial sequence

<220>
 <223> Obtained N-terminal sequence of 36/41 derived VL prod. in Corn
 <400> 78

Leu Val Leu Thr Gln Ser Pro Ala Ile
 1 5

<210> 79
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> Predicted N-terminal sequence of 36/41 derived VH in corn
 <400> 79

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 1 5 10

<210> 80
 <211> 10
 <212> PRT
 <213> artificial sequence

<220>
 <223> obtained N-terminal sequence of 36/41 derived VH in corn

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> Xaa can be any naturally occurring amino acid
 <400> 80

Glu Xaa Gln Leu Gln Gln Ser Gly Pro Glu

corrected 70235USPCT.ST25
10

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5